

SEQUENCE LISTING

5

(1) GENERAL INFORMATION:

(i) APPLICANT: Sato, Takaaki

10 (ii) TITLE OF INVENTION: TREX, A NOVEL GENE OF TRAF-INTERACTING
EXT GENE FAMILY AND DIAGNOSTIC AND THERAPEUTIC USES
THEREOF

(iii) NUMBER OF SEQUENCES: 37

15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Cooper & Dunham LLP
(B) STREET: 1185 Avenue of the Americas
(C) CITY: New York
20 (D) STATE: New York
(E) COUNTRY: U.S.A
(F) ZIP: 10036

(v) COMPUTER READABLE FORM:

25

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

30 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

35 (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: White, John P.
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 0575/51902-A-PCT

40 (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 278-0400
(B) TELEFAX: (212) 391-0525

45 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3479 base pairs
(B) TYPE: nucleic acid
50 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

55

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 458..3211

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

05809920-031601

	CCTGATCGTT	GGTAGTGGCA	TGGAGGACGG	GGCTGGCATT	TCAGACTGCC	AGCTGTTTTT	60
	ACCAGCCGCT	GCATCACTTG	AATAGAAGCT	ATGCATATTG	GCTGGCCGAC	AAAGCCAAGG	120
	5GACAAAAGCT	ATGGCCGTTA	AAATGGTCCC	TCTGAGTCCA	GGGCTCTTTC	CCTGGCTTTT	180
	AGCACCATGG	ATCTCTTCCT	TTTCATCCCA	TCAGCAATGT	GGTACCTTCT	TCTACTTGAT	240
	GATGACAGCT	GATACTTCAG	ATTTGCCTGA	CTAAGGTTAG	AAACCTGAAT	CGCTGTGAGG	300
10	AAGATGAAAT	TTCCATTTTA	CTTGGTGCCT	TGTGCAGGGA	GCACACTGAT	CCTTCCAGAA	360
	ACTTGTGTGT	GAAAAGAGGT	TGCGTTTTGT	CAGACAGACT	CATGGTTATG	GCGAGCGATC	420
15	CGACGTGATC	AGAGTGGGCA	AGAGGCACAG	CGAACTC	ATG ACA GGC TAT ACC ATG		475
					Met Thr Gly Tyr Thr Met		
					1 5		
	TTG CGG AAT GGG GGA GTG GGG AAC GGT GGT CAG ACC TGT ATG CTG CGC						523
20	Leu Arg Asn Gly Gly Val Gly Asn Gly Gly Gln Thr Cys Met Leu Arg						
		10		15		20	
	TGG TCC AAT CGC ATC CGG CTG ACA TGG CTG AGT TTC ACG CTG TTC ATC						571
25	Trp Ser Asn Arg Ile Arg Leu Thr Trp Leu Ser Phe Thr Leu Phe Ile						
		25		30		35	
	ATC CTC GTC TTC TTC CCC CTC ATT GCT CAC TAT TAC CTC ACC ACT CTG						619
30	Ile Leu Val Phe Phe Pro Leu Ile Ala His Tyr Tyr Leu Thr Thr Leu						
		40		45		50	
	GAC GAG GCA GAC GAG GCT GGC AAG CGC ATC TTC GGC CCT CGG GCT GGC						667
	Asp Glu Ala Asp Glu Ala Gly Lys Arg Ile Phe Gly Pro Arg Ala Gly						
		55		60		65	70
35	AGT GAG CTC TGT GAG GTA AAG CAT GTC CTT GAT CTC TGT CGG ATT CGT						715
	Ser Glu Leu Cys Glu Val Lys His Val Leu Asp Leu Cys Arg Ile Arg						
			75			80	85
	GAG TCT GTG AGC GAA GAG CTT CTA CAG CTC GAA GCC AAG CGG CAG GAG						763
40	Glu Ser Val Ser Glu Glu Leu Leu Gln Leu Glu Ala Lys Arg Gln Glu						
			90			95	100
	CTG AAC AGC GAG ATT GCC AAG CTG AAC CTC AAG ATT GAA GCC TGT AAG						811
45	Leu Asn Ser Glu Ile Ala Lys Leu Asn Leu Lys Ile Glu Ala Cys Lys						
		105				110	115
	AAG AGC ATA GAG AAT GCC AAG CAG GAC CTG CTG CAG CTC AAG AAT GTC						859
50	Lys Ser Ile Glu Asn Ala Lys Gln Asp Leu Leu Gln Leu Lys Asn Val						
		120				125	130
	ATT AGC CAG ACA GAG CAC TCC TAC AAG GAG CTG ATG GCC CAG AAC CAG						907
	Ile Ser Gln Thr Glu His Ser Tyr Lys Glu Leu Met Ala Gln Asn Gln						
				140		145	150
55	CCC AAA CTG TCC CTG CCC ATC CGA CTG CTC CCT GAG AAG GAC GAT GCC						955
	Pro Lys Leu Ser Leu Pro Ile Arg Leu Leu Pro Glu Lys Asp Asp Ala						
			155			160	165
	GGC CTT CCA CCC CCC AAG GTC ACT CGG GGT TGC CGC CTT CAC AAC TGC						1003
60	Gly Leu Pro Pro Pro Lys Val Thr Arg Gly Cys Arg Leu His Asn Cys						
			170			175	180
	TTT GAT TAC TCT CGT TGT CCT CTG ACG TCT GGC TTT CCC GTC TAC GTC						1051

	Phe	Asp	Tyr	Ser	Arg	Cys	Pro	Leu	Thr	Ser	Gly	Phe	Pro	Val	Tyr	Val	
		185						190					195				
	TAT	GAC	AGT	GAC	CAG	TTT	GCC	TTT	GGG	AGC	TAC	CTG	GAC	CCT	TTG	GTC	1099
5	Tyr	Asp	Ser	Asp	Gln	Phe	Ala	Phe	Gly	Ser	Tyr	Leu	Asp	Pro	Leu	Val	
		200					205					210					
	AAG	CAG	GCT	TTT	CAG	GCT	ACA	GTG	AGA	GCC	AAC	GTT	TAT	GTT	ACA	GAA	1147
10	Lys	Gln	Ala	Phe	Gln	Ala	Thr	Val	Arg	Ala	Asn	Val	Tyr	Val	Thr	Glu	
215						220					225					230	
	AAT	GCG	GCC	ATC	GCC	TGC	CTG	TAT	GTG	GTG	TTA	GTG	GGA	GAA	ATG	CAA	1195
	Asn	Ala	Ala	Ile	Ala	Cys	Leu	Tyr	Val	Val	Leu	Val	Gly	Glu	Met	Gln	
					235					240					245		
15	GAG	CCC	ACT	GTG	CTG	CGG	CCT	GCC	GAC	CTT	GAA	AAG	CAG	CTG	TTT	TCT	1243
	Glu	Pro	Thr	Val	Leu	Arg	Pro	Ala	Asp	Leu	Glu	Lys	Gln	Leu	Phe	Ser	
				250					255					260			
20	CTG	CCA	CAC	TGG	AGG	ACA	GAT	GGG	CAC	AAC	CAC	GTC	ATT	ATC	AAC	CTG	1291
	Leu	Pro	His	Trp	Arg	Thr	Asp	Gly	His	Asn	His	Val	Ile	Ile	Asn	Leu	
			265					270					275				
	TCC	CGG	AAG	TCA	GAC	ACA	CAG	AAT	CTA	CTG	TAC	AAC	GTC	AGT	ACA	GGC	1339
25	Ser	Arg	Lys	Ser	Asp	Thr	Gln	Asn	Leu	Leu	Tyr	Asn	Val	Ser	Thr	Gly	
		280					285					290					
	CGC	CAT	GTG	GCC	CAG	TCC	ACC	CTC	TAT	GCT	GCC	CAG	TAC	AGA	GCT	GGC	1387
30	Arg	His	Val	Ala	Gln	Ser	Thr	Leu	Tyr	Ala	Ala	Gln	Tyr	Arg	Ala	Gly	
295						300					305					310	
	TTT	GAC	CTG	GTC	GTG	TCA	CCC	CTT	GTC	CAT	GCT	ATG	TCT	GAA	CCC	AAC	1435
	Phe	Asp	Leu	Val	Val	Ser	Pro	Leu	Val	His	Ala	Met	Ser	Glu	Pro	Asn	
					315					320					325		
35	TTC	ATG	GAA	ATC	CCA	CCG	CAG	GTG	CCA	GTT	AAG	CGG	AAA	TAT	CTC	TTC	1483
	Phe	Met	Glu	Ile	Pro	Pro	Gln	Val	Pro	Val	Lys	Arg	Lys	Tyr	Leu	Phe	
				330					335					340			
40	ACT	TTC	CAG	GGC	GAG	AAG	ATC	GAG	TCT	CTG	AGA	TCT	AGC	CTT	CAG	GAG	1531
	Thr	Phe	Gln	Gly	Glu	Lys	Ile	Glu	Ser	Leu	Arg	Ser	Ser	Leu	Gln	Glu	
			345					350					355				
	GCC	CGT	TCC	TTC	GAG	GAA	GAG	ATG	GAG	GGC	GAC	CCT	CCG	GCC	GAC	TAT	1579
45	Ala	Arg	Ser	Phe	Glu	Glu	Glu	Met	Glu	Gly	Asp	Pro	Pro	Ala	Asp	Tyr	
		360					365					370					
	GAC	GAT	CGC	ATC	ATT	GCC	ACC	CTA	AAG	GCT	GTA	CAG	GAC	AGC	AAG	CTG	1627
50	Asp	Asp	Arg	Ile	Ile	Ala	Thr	Leu	Lys	Ala	Val	Gln	Asp	Ser	Lys	Leu	
375						380					385					390	
	GAT	CAG	GTG	CTG	GTA	GAA	TTC	ACT	TGC	AAA	AAC	CAG	CCG	AAG	CCT	AGC	1675
	Asp	Gln	Val	Leu	Val	Glu	Phe	Thr	Cys	Lys	Asn	Gln	Pro	Lys	Pro	Ser	
					395					400					405		
55	CTG	CCG	ACT	GAG	TGG	GCA	CTG	TGT	GGG	GAG	CGG	GAA	GAC	CGC	CTG	GAG	1723
	Leu	Pro	Thr	Glu	Trp	Ala	Leu	Cys	Gly	Glu	Arg	Glu	Asp	Arg	Leu	Glu	
				410					415					420			
60	TTA	CTG	AAG	CTC	TCC	ACC	TTC	GCC	CTC	ATC	ATC	ACT	CCC	GGG	GAC	CCG	1771
	Leu	Leu	Lys	Leu	Ser	Thr	Phe	Ala	Leu	Ile	Ile	Thr	Pro	Gly	Asp	Pro	
			425					430					435				

00809920 031601

CGC	CTG	CTC	ATT	TCA	TCT	GGG	TGT	GCC	ACG	CGG	CTC	TTC	GAG	GCC	CTG	1819
Arg	Leu	Leu	Ile	Ser	Ser	Gly	Cys	Ala	Thr	Arg	Leu	Phe	Glu	Ala	Leu	
440						445					450					
5GAG	GTG	GGG	GCC	GTG	CCG	GTG	GTG	CTC	GGG	GAG	CAG	GTG	CAG	CTC	CCG	1867
Glu	Val	Gly	Ala	Val	Pro	Val	Val	Leu	Gly	Glu	Gln	Val	Gln	Leu	Pro	
455					460					465					470	
TAC	CAC	GAC	ATG	CTG	CAG	TGG	AAC	GAG	GCC	GCC	CTG	GTG	GTG	CCC	AAG	1915
10Tyr	His	Asp	Met	Leu	Gln	Trp	Asn	Glu	Ala	Ala	Leu	Val	Val	Pro	Lys	
				475					480					485		
CCT	CGC	GTC	ACA	GAG	GTC	CAC	TTC	CTG	TTA	CGA	AGT	CTT	TCA	GAC	AGT	1963
Pro	Arg	Val	Thr	Glu	Val	His	Phe	Leu	Leu	Arg	Ser	Leu	Ser	Asp	Ser	
15			490					495					500			
GAT	CTG	TTG	GCC	ATG	AGG	CGG	CAA	GGC	CGC	TTT	CTC	TGG	GAG	ACC	TAC	2011
Asp	Leu	Leu	Ala	Met	Arg	Arg	Gln	Gly	Arg	Phe	Leu	Trp	Glu	Thr	Tyr	
		505					510					515				
20																
TTC	TCC	ACC	GCA	GAC	AGT	ATT	TTT	AAT	ACC	GTG	CTG	GCC	ATG	ATT	AGG	2059
Phe	Ser	Thr	Ala	Asp	Ser	Ile	Phe	Asn	Thr	Val	Leu	Ala	Met	Ile	Arg	
	520					525					530					
25ACT	CGA	ATT	CAG	ATC	CCA	GCT	GCT	CCC	ATC	CGG	GAA	GAG	GTA	GCG	GCT	2107
Thr	Arg	Ile	Gln	Ile	Pro	Ala	Ala	Pro	Ile	Arg	Glu	Glu	Val	Ala	Ala	
535					540					545					550	
GAG	ATC	CCC	CAT	CGT	TCA	GGC	AAA	GCA	GCT	GGA	ACT	GAC	CCC	AAC	ATG	2155
30Glu	Ile	Pro	His	Arg	Ser	Gly	Lys	Ala	Ala	Gly	Thr	Asp	Pro	Asn	Met	
			555					560						565		
GCT	GAC	AAT	GGG	GAC	CTG	GAC	CTG	GGG	CCG	GTA	GAG	ACA	GAA	CCA	CCC	2203
Ala	Asp	Asn	Gly	Asp	Leu	Asp	Leu	Gly	Pro	Val	Glu	Thr	Glu	Pro	Pro	
35			570					575					580			
TAT	GCC	TCA	CCT	AAA	TAC	CTC	CGC	AAT	TTC	ACT	CTG	ACT	GTC	ACA	GAC	2251
Tyr	Ala	Ser	Pro	Lys	Tyr	Leu	Arg	Asn	Phe	Thr	Leu	Thr	Val	Thr	Asp	
		585					590					595				
40																
TGT	TAC	CGT	GGC	TGG	AAC	TCT	GCC	CCG	GGA	CGG	TTC	CAT	CTT	TTT	CCC	2299
Cys	Tyr	Arg	Gly	Trp	Asn	Ser	Ala	Pro	Gly	Arg	Phe	His	Leu	Phe	Pro	
	600					605					610					
45CAC	ACA	CCC	TTT	GAT	CCT	GTG	TTG	CCC	TCT	GAG	GCC	AAA	TTC	TTG	GGC	2347
His	Thr	Pro	Phe	Asp	Pro	Val	Leu	Pro	Ser	Glu	Ala	Lys	Phe	Leu	Gly	
615					620					625					630	
TCA	GGG	ACT	GGA	TTT	CGG	CCG	ATC	GGT	GGC	GGG	GCT	GGG	GGC	TCT	GGC	2395
50Ser	G															

	TGG	AAC	TCT	CCC	AAG	CTG	CCC	TCG	GAG	GAC	CTT	TTG	TGG	CCA	GAC	ATT	2587
	Trp	Asn	Ser	Pro	Lys	Leu	Pro	Ser	Glu	Asp	Leu	Leu	Trp	Pro	Asp	Ile	
	695					700					705					710	
5	GGT	GTC	CCC	ATC	ATG	GTC	GTC	CGT	ACT	GAG	AAG	AAC	AGT	TTG	AAC	AAT	2635
	Gly	Val	Pro	Ile	Met	Val	Val	Arg	Thr	Glu	Lys	Asn	Ser	Leu	Asn	Asn	
					715					720					725		
	CGG	TTC	TTG	CCC	TGG	AAT	GAG	ATT	GAG	ACA	GAG	GCC	ATA	CTG	TCC	ATC	2683
10	Arg	Phe	Leu	Pro	Trp	Asn	Glu	Ile	Glu	Thr	Glu	Ala	Ile	Leu	Ser	Ile	
				730					735					740			
	GAC	GAT	GAT	GCT	CAC	CTC	CGC	CAT	GAT	GAA	ATC	ATG	TTT	GGG	TTT	TGG	2731
15	Asp	Asp	Asp	Ala	His	Leu	Arg	His	Asp	Glu	Ile	Met	Phe	Gly	Phe	Trp	
			745					750					755				
	GTG	TGG	AGA	GAA	GCA	CGT	GAT	CGC	ATT	GTG	GGT	TTC	CCT	GGC	CGG	TAC	2779
	Val	Trp	Arg	Glu	Ala	Arg	Asp	Arg	Ile	Val	Gly	Phe	Pro	Gly	Arg	Tyr	
		760					765					770					
20	CAT	GCG	TGG	GAC	ATC	CCG	CAC	CAG	TCC	TGG	CTC	TAC	AAT	TCC	AAC	TAC	2827
	His	Ala	Trp	Asp	Ile	Pro	His	Gln	Ser	Trp	Leu	Tyr	Asn	Ser	Asn	Tyr	
	775					780					785					790	
25	TCC	TGT	GAG	CTG	TCC	ATG	GTG	CTG	ACG	GGC	GCT	GCC	TTC	TTT	CAC	AAG	2875
	Ser	Cys	Glu	Leu	Ser	Met	Val	Leu	Thr	Gly	Ala	Ala	Phe	Phe	His	Lys	
					795					800					805		
	TAT	TAT	GCC	TAC	CTG	TAT	TCT	TAT	GTG	ATG	CCC	CAG	GCC	ATC	CGG	GAC	2923
30	Tyr	Tyr	Ala	Tyr	Leu	Tyr	Ser	Tyr	Val	Met	Pro	Gln	Ala	Ile	Arg	Asp	
				810					815					820			
	ATG	GTG	GAC	GAG	TAC	ATC	AAC	TGT	GAG	GAT	ATC	GCC	ATG	AAC	TTC	CTT	2971
	Met	Val	Asp	Glu	Tyr	Ile	Asn	Cys	Glu	Asp	Ile	Ala	Met	Asn	Phe	Leu	
35			825					830					835				
	GTC	TCC	CAC	ATC	ACA	CGG	AAA	CCC	CCC	ATC	AAG	GTG	ACA	TCA	AGG	TGG	3019
	Val	Ser	His	Ile	Thr	Arg	Lys	Pro	Pro	Ile	Lys	Val	Thr	Ser	Arg	Trp	
			840				845					850					
40	ACT	TTT	CGA	TGC	CCA	GGG	TGC	CCT	CAG	GCC	CTG	TCC	CAT	GAT	GAC	TCT	3067
	Thr	Phe	Arg	Cys	Pro	Gly	Cys	Pro	Gln	Ala	Leu	Ser	His	Asp	Asp	Ser	
	855					860					865					870	
45	CAT	TTT	CAC	GAG	CGG	CAC	AAG	TGT	ATC	AAC	TTT	TTT	GTC	AAG	GTG	TAC	3115
	His	Phe	His	Glu	Arg	His	Lys	Cys	Ile	Asn	Phe	Phe	Val	Lys	Val	Tyr	
					875					880					885		
	GGC	TAT	ATG	CCT	CTC	TTG	TAC	ACA	CAG	TTC	AGG	GTG	GAC	TCC	GTG	CTC	3163
50	Gly	Tyr	Met	Pro													

ACTGAGGACT GTTCATAAGC CCAGGACA

3479

(2) INFORMATION FOR SEQ ID NO:2:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 918 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

15Met Thr Gly Tyr Thr Met Leu Arg Asn Gly Gly Val Gly Asn Gly Gly
 1 5 10 15
 Gln Thr Cys Met Leu Arg Trp Ser Asn Arg Ile Arg Leu Thr Trp Leu
 20 25 30
 20Ser Phe Thr Leu Phe Ile Ile Leu Val Phe Phe Pro Leu Ile Ala His
 35 40 45
 Tyr Tyr Leu Thr Thr Leu Asp Glu Ala Asp Glu Ala Gly Lys Arg Ile
 25 50 55 60
 Phe Gly Pro Arg Ala Gly Ser Glu Leu Cys Glu Val Lys His Val Leu
 65 70 75 80
 30Asp Leu Cys Arg Ile Arg Glu Ser Val Ser Glu Glu Leu Leu Gln Leu
 85 90 95
 Glu Ala Lys Arg Gln Glu Leu Asn Ser Glu Ile Ala Lys Leu Asn Leu
 100 105 110
 35Lys Ile Glu Ala Cys Lys Lys Ser Ile Glu Asn Ala Lys Gln Asp Leu
 115 120 125
 Leu Gln Leu Lys Asn Val Ile Ser Gln Thr Glu His Ser Tyr Lys Glu
 40 130 135 140
 Leu Met Ala Gln Asn Gln Pro Lys Leu Ser Leu Pro Ile Arg Leu Leu
 145 150 155 160
 45Pro Glu Lys Asp Asp Ala Gly Leu Pro Pro Pro Lys Val Thr Arg Gly
 165 170 175
 Cys Arg Leu His Asn Cys Phe Asp Tyr Ser Arg Cys Pro Leu Thr Ser
 180 185 190
 50Gly Phe Pro Val Tyr Val Tyr Asp Ser Asp Gln Phe Ala Phe Gly Ser
 195 200 205
 Tyr Leu Asp Pro Leu Val Lys Gln Ala Phe Gln Ala Thr Val Arg Ala
 55 210 215 220
 Asn Val Tyr Val Thr Glu Asn Ala Ala Ile Ala Cys Leu Tyr Val Val
 225 230 235 240
 60Leu Val Gly Glu Met Gln Glu Pro Thr Val Leu Arg Pro Ala Asp Leu
 245 250 255
 Glu Lys Gln Leu Phe Ser Leu Pro His Trp Arg Thr Asp Gly His Asn

TOLEO-02560850

	260	265	270
	His Val Ile Ile Asn Leu Ser Arg Lys Ser Asp Thr Gln Asn Leu Leu 275 280 285		
5	Tyr Asn Val Ser Thr Gly Arg His Val Ala Gln Ser Thr Leu Tyr Ala 290 295 300		
10	Ala Gln Tyr Arg Ala Gly Phe Asp Leu Val Val Ser Pro Leu Val His 305 310 315 320		
	Ala Met Ser Glu Pro Asn Phe Met Glu Ile Pro Pro Gln Val Pro Val 325 330 335		
15	Lys Arg Lys Tyr Leu Phe Thr Phe Gln Gly Glu Lys Ile Glu Ser Leu 340 345 350		
	Arg Ser Ser Leu Gln Glu Ala Arg Ser Phe Glu Glu Glu Met Glu Gly 355 360 365		
20	Asp Pro Pro Ala Asp Tyr Asp Asp Arg Ile Ile Ala Thr Leu Lys Ala 370 375 380		
	Val Gln Asp Ser Lys Leu Asp Gln Val Leu Val Glu Phe Thr Cys Lys 385 390 395 400		
	Asn Gln Pro Lys Pro Ser Leu Pro Thr Glu Trp Ala Leu Cys Gly Glu 405 410 415		
30	Arg Glu Asp Arg Leu Glu Leu Leu Lys Leu Ser Thr Phe Ala Leu Ile 420 425 430		
	Ile Thr Pro Gly Asp Pro Arg Leu Leu Ile Ser Ser Gly Cys Ala Thr 435 440 445		
35	Arg Leu Phe Glu Ala Leu Glu Val Gly Ala Val Pro Val Val Leu Gly 450 455 460		
	Glu Gln Val Gln Leu Pro Tyr His Asp Met Leu Gln Trp Asn Glu Ala 465 470 475 480		
	Ala Leu Val Val Pro Lys Pro Arg Val Thr Glu Val His Phe Leu Leu 485 490 495		
45	Arg Ser Leu Ser Asp Ser Asp Leu Leu Ala Met Arg Arg Gln Gly Arg 500 505 510		
	Phe Leu Trp Glu Thr Tyr Phe Ser Thr Ala Asp Ser Ile Phe Asn Thr 515 520 525		
50	Val Leu Ala Met Ile Arg Thr Arg Ile Gln Ile Pro Ala Ala Pro Ile 530 535 540		
	Arg Glu Glu Val Ala Ala Glu Ile Pro His Arg Ser Gly Lys Ala Ala 545 550 555 560		
	Gly Thr Asp Pro Asn Met Ala Asp Asn Gly Asp Leu Asp Leu Gly Pro 565 570 575		
60	Val Glu Thr Glu Pro Pro Tyr Ala Ser Pro Lys Tyr Leu Arg Asn Phe 580 585 590		
	Thr Leu Thr Val Thr Asp Cys Tyr Arg Gly Trp Asn Ser Ala Pro Gly		

595 600 605
 Arg Phe His Leu Phe Pro His Thr Pro Phe Asp Pro Val Leu Pro Ser
 610 615 620
 5
 Glu Ala Lys Phe Leu Gly Ser Gly Thr Gly Phe Arg Pro Ile Gly Gly
 625 630 635 640
 Gly Ala Gly Gly Ser Gly Lys Glu Phe Gln Ala Ala Leu Gly Gly Asn
 10 645 650 655
 Val Gln Arg Glu Gln Phe Thr Val Val Met Leu Thr Tyr Glu Arg Glu
 660 665 670
 15 Glu Val Leu Met Asn Ser Leu Glu Arg Leu Asn Gly Leu Pro Tyr Leu
 675 680 685
 Asn Lys Val Val Val Val Trp Asn Ser Pro Lys Leu Pro Ser Glu Asp
 690 695 700
 20
 Leu Leu Trp Pro Asp Ile Gly Val Pro Ile Met Val Val Arg Thr Glu
 705 710 715 720
 Lys Asn Ser Leu Asn Asn Arg Phe Leu Pro Trp Asn Glu Ile Glu Thr
 25 725 730 735
 Glu Ala Ile Leu Ser Ile Asp Asp Ala His Leu Arg His Asp Glu
 740 745 750
 30 Ile Met Phe Gly Phe Trp Val Trp Arg Glu Ala Arg Asp Arg Ile Val
 755 760 765
 Gly Phe Pro Gly Arg Tyr His Ala Trp Asp Ile Pro His Gln Ser Trp
 770 775 780
 35
 Leu Tyr Asn Ser Asn Tyr Ser Cys Glu Leu Ser Met Val Leu Thr Gly
 785 790 795 800
 Ala Ala Phe Phe His Lys Tyr Tyr Ala Tyr Leu Tyr Ser Tyr Val Met
 40 805 810 815
 Pro Gln Ala Ile Arg Asp Met Val Asp Glu Tyr Ile Asn Cys Glu Asp
 820 825 830
 45 Ile Ala Met Asn Phe Leu Val Ser His Ile Thr Arg Lys Pro Pro Ile
 835 840 845
 Lys Val Thr Ser Arg Trp Thr Phe Arg Cys Pro Gly Cys Pro Gln Ala
 850 855 860
 50
 Leu Ser His Asp Asp Ser His Phe His Glu Arg His Lys Cys Ile Asn
 865 870 875 880
 Phe Phe Val Lys Val Tyr Gly Tyr Met Pro Leu Leu Tyr Thr Gln Phe
 55 885 890 895
 Arg Val Asp Ser Val Leu Phe Lys Thr Arg Leu Pro His Asp Lys Thr
 900 905 910
 60 Lys Cys Phe Lys Phe Ile
 915

(2) INFORMATION FOR SEQ ID NO:3:

09809920.031601

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6172 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 594..3350

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCGGGTCCC TGAGCTGGAA GCCGGAGAGC AAGCCCTGGA GGTTCACTCT TTCAAGAAGT 60
 CGTGTGCTGA GGTGTAATGC TACACAAGTC AGAGGAAGGA AGGGTCCTGA AACACATGGC 120
 20 CTGATTGTTG GCAAAGGCAT CATAAGAAGC TGGCATTAT TTCTGTTCTA ACCTATTACT 180
 GTATAACTGT GAATAGACAC TATGCATATT TGTTGGTCAG CAAAACCAAG AAACAAGAGC 240
 25 TATGGCATT T GAAAAAGTCT GTCTGATTCC AGGGTGTTTT TCCTGGGTTT CATCATCAGG 300
 TACCTCCTCC CTTTCATCTC AGCAAGAATG TGGCACCTTT TATCGTTTGA TAAAGATTAA 360
 GGACATGTTT TTTGGTCAAC AGCCAGAACT TAAATCTGC TGGAATAGGG TCAGAGACCA 420
 30 TTTCAGCTGC AGCTGAGGAA AATGAAATGT TCATTTTATT TGGTGCCTTG TCTGGGGAGC 480
 AACTAACTC TTCTGGAAAC GTGTCAGTGA AACAGAGATC GTTTTGTGGA ATAGCAACCC 540
 35 ATGGTTATGG CGAGTGACCC GACGTGATCT GGGGGGCAGG CTGCAGAGGA CTC ATG 596
 Met
 ACA GGC TAT ACC ATG CTG CGG AAT GGG GGC GCG GGG AAC GGA GGT CAG 644
 40 Thr Gly Tyr Thr Met Leu Arg Asn Gly Gly Ala Gly Asn Gly Gly Gln 920 925 930 935
 ACC TGC ATG CTG CGC TGG TCC AAC CGC ATC CGC CTC ACG TGG CTC AGC 692
 45 Thr Cys Met Leu Arg Trp Ser Asn Arg Ile Arg Leu Thr Trp Leu Ser 940 945 950
 TTC ACG CTC TTT GTC ATC CTG GTC TTC TTC CCG CTC ATC GCC CAC TAT 740
 Phe Thr Leu Phe Val Ile Leu Val Phe Phe Pro Leu Ile Ala His Tyr 955 960 965
 50 TAC CTC ACC ACT CTG GAT GAG GCT GAT GAG GCA GGC AAG CGG ATT TTT 788
 Tyr Leu Thr Thr Leu Asp Glu Ala Asp Glu Ala Gly Lys Arg Ile Phe 970 975 980
 55 GGT CCC CGG GTG GGG AAC GAG CTG TGC GAG GTG AAG CAC GTG CTG GAT 836
 Gly Pro Arg Val Gly Asn Glu Leu Cys Glu Val Lys His Val Leu Asp 985 990 995
 CTG TGC CGC ATC CGG GAG TCG GTG AGT GAA GAG CTC CTG CAG CTG GAG 884
 60 Leu Cys Arg Ile Arg Glu Ser Val Ser Glu Glu Leu Leu Gln Leu Glu 1000 1005 1010 1015
 GCC AAG CGC CAA GAG CTG AAC AGC GAG ATC GCC AAG CTG AAT CTG AAG 932

TOTAL: 02660860

	Ala	Lys	Arg	Gln	Glu	Leu	Asn	Ser	Glu	Ile	Ala	Lys	Leu	Asn	Leu	Lys	
					1020					1025					1030		
	ATC	GAA	GCC	TGT	AAG	AAG	AGC	ATT	GAG	AAC	GCC	AAG	CAG	GAC	CTG	CTC	980
5	Ile	Glu	Ala	Cys	Lys	Lys	Ser	Ile	Glu	Asn	Ala	Lys	Gln	Asp	Leu	Leu	
				1035					1040					1045			
	CAG	CTC	AAG	AAT	GTC	ATC	AGC	CAG	ACC	GAG	CAT	TCC	TAC	AAG	GAG	CTC	1028
10	Gln	Leu	Lys	Asn	Val	Ile	Ser	Gln	Thr	Glu	His	Ser	Tyr	Lys	Glu	Leu	
			1050					1055					1060				
	ATG	GCC	CAG	AAC	CAG	CCC	AAG	CTG	TCC	CTG	CCC	ATC	CGA	CTG	CTC	CCA	1076
	Met	Ala	Gln	Asn	Gln	Pro	Lys	Leu	Ser	Leu	Pro	Ile	Arg	Leu	Leu	Pro	
		1065					1070					1075					
15	GAG	AAG	GAC	GAT	GCC	GGC	CTC	CCT	CCC	CCG	AAG	GCC	ACT	CGG	GGC	TGC	1124
	Glu	Lys	Asp	Asp	Ala	Gly	Leu	Pro	Pro	Pro	Lys	Ala	Thr	Arg	Gly	Cys	
		1080				1085					1090					1095	
20	CGG	CTA	CAC	AAC	TGC	TTT	GAT	TAT	TCT	CGT	TGC	CCT	CTC	ACC	TCT	GGC	1172
	Arg	Leu	His	Asn	Cys	Phe	Asp	Tyr	Ser	Arg	Cys	Pro	Leu	Thr	Ser	Gly	
				1100						1105					1110		
	TTC	CCG	GTC	TAC	GTC	TAT	GAC	AGT	GAC	CAG	TTT	GTC	TTT	GGC	AGC	TAC	1220
25	Phe	Pro	Val	Tyr	Val	Tyr	Asp	Ser	Asp	Gln	Phe	Val	Phe	Gly	Ser	Tyr	
				1115					1120					1125			
	CTG	GAT	CCC	TTG	GTC	AAG	CAG	GCT	TTT	CAG	GCG	ACA	GCA	CGA	GCT	AAC	1268
30	Leu	Asp	Pro	Leu	Val	Lys	Gln	Ala	Phe	Gln	Ala	Thr	Ala	Arg	Ala	Asn	
			1130				1135						1140				
	GTT	TAT	GTT	ACA	GAA	AAT	GCA	GAC	ATC	GCC	TGC	CTT	TAC	GTG	ATA	CTA	1316
	Val	Tyr	Val	Thr	Glu	Asn	Ala	Asp	Ile	Ala	Cys	Leu	Tyr	Val	Ile	Leu	
		1145				1150						1155					
35	GTG	GGA	GAG	ATG	CAG	GAG	CCC	GTG	GTG	CTG	CGG	CCT	GCT	GAG	CTG	GAG	1364
	Val	Gly	Glu	Met	Gln	Glu	Pro	Val	Val	Leu	Arg	Pro	Ala	Glu	Leu	Glu	
		1160				1165					1170					1175	
40	AAG	CAG	TTG	TAT	TCC	CTG	CCA	CAC	TGG	CGG	ACG	GAT	GGA	CAC	AAC	CAT	1412
	Lys	Gln	Leu	Tyr	Ser	Leu	Pro	His	Trp	Arg	Thr	Asp	Gly	His	Asn	His	
				1180						1185					1190		
	GTC	ATC	ATC	AAT	CTG	TCA	CGT	AAG	TCA	GAT	ACA	CAG	AAC	CTT	CTC	TAT	1460
45	Val	Ile	Ile	Asn	Leu	Ser	Arg	Lys	Ser	Asp	Thr	Gln	Asn	Leu	Leu	Tyr	
				1195					1200					1205			
	AAC	GTC	AGT	ACT	GGC	CGT	GCC	ATG	GTG	GCC	CAG	TCC	ACC	TTC	TAC	ACT	1508
50	Asn	Val	Ser	Thr	Gly	Arg	Ala	Met	Val	Ala	Gln	Ser	Thr	Phe	Tyr	Thr	
			1210					1215					1220				
	GTC	CAG	TAC	AGA	CCT	GGC	TTT	GAC	TTG	GTC	GTA	TCA	CCG	CTG	GTC	CAT	1556
	Val	Gln	Tyr	Arg	Pro	Gly	Phe	Asp	Leu	Val	Val	Ser	Pro	Leu	Val	His	
		1225				1230						1235					
55	GCC	ATG	TCT	GAG	CCC	AAC	TTC	ATG	GAA	ATC	CCA	CCA	CAG	GTG	CCG	GTG	1604
	Ala	Met	Ser	Glu	Pro	Asn	Phe	Met	Glu	Ile	Pro	Pro	Gln	Val	Pro	Val	
		1240				1245					1250					1255	
60	AAG	CGG	AAA	TAT	CTC	TTC	ACC	TTC	CAG	GGC	GAG	AAG	ATT	GAG	TCT	CTG	1652
	Lys	Arg	Lys	Tyr	Leu	Phe	Thr	Phe	Gln	Gly	Glu	Lys	Ile	Glu	Ser	Leu	
				1260						1265					1270		

TOTAL: 02660860

	AGG	TCT	AGC	CTT	CAG	GAG	GCC	CGC	TCC	TTC	GAA	GAG	GAA	ATG	GAG	GGC	1700
	Arg	Ser	Ser	Leu	Gln	Glu	Ala	Arg	Ser	Phe	Glu	Glu	Glu	Met	Glu	Gly	
				1275					1280					1285			
	5GAC	CCT	CCC	GCC	GAC	TAC	GAT	GAC	CGG	ATC	ATT	GCC	ACC	CTG	AAG	GCG	1748
	Asp	Pro	Pro	Ala	Asp	Tyr	Asp	Asp	Arg	Ile	Ile	Ala	Thr	Leu	Lys	Ala	
			1290					1295					1300				
	GTG	CAG	GAC	AGC	AAG	CTG	GAT	CAG	GTC	CTG	GTG	GAA	TTC	ACC	TGC	AAA	1796
10	Val	Gln	Asp	Ser	Lys	Leu	Asp	Gln	Val	Leu	Val	Glu	Phe	Thr	Cys	Lys	
		1305					1310					1315					
	AAC	CAG	CCC	AAA	CCC	AGC	CTG	CCG	ACT	GAG	TGG	GCA	CTG	TGT	GGA	GAG	1844
	Asn	Gln	Pro	Lys	Pro	Ser	Leu	Pro	Thr	Glu	Trp	Ala	Leu	Cys	Gly	Glu	
15	1320					1325				1330						1335	
	CGG	GAG	GAC	CGC	TTG	GAA	TTG	CTG	AAG	CTC	TCC	ACC	TTC	GCC	CTC	ATC	1892
	Arg	Glu	Asp	Arg	Leu	Glu	Leu	Leu	Lys	Leu	Ser	Thr	Phe	Ala	Leu	Ile	
				1340						1345					1350		
20	ATT	ACC	CCC	GGG	GAC	CCT	CGC	TTG	GTT	ATT	TCC	TCT	GGG	TGT	GCA	ACA	1940
	Ile	Thr	Pro	Gly	Asp	Pro	Arg	Leu	Val	Ile	Ser	Ser	Gly	Cys	Ala	Thr	
				1355				1360						1365			
	25CGG	CTC	TTC	GAA	GCC	CTG	GAA	GTC	GGT	GCC	GTC	CCG	GTG	GTG	CTG	GGG	1988
	Arg	Leu	Phe	Glu	Ala	Leu	Glu	Val	Gly	Ala	Val	Pro	Val	Val	Leu	Gly	
			1370					1375				1380					
	GAG	CAG	GTC	CAG	CTT	CCC	TAC	CAG	GAC	ATG	CTG	CAG	TGG	AAC	GAG	GCG	2036
30	Glu	Gln	Val	Gln	Leu	Pro	Tyr	Gln	Asp	Met	Leu	Gln	Trp	Asn	Glu	Ala	
		1385					1390					1395					
	GCC	CTG	GTG	GTG	CCA	AAG	CCT	CGT	GTT	ACC	GAG	GTT	CAT	TTC	CTG	CTC	2084
	Ala	Leu	Val	Val	Pro	Lys	Pro	Arg	Val	Thr	Glu	Val	His	Phe	Leu	Leu	
35	1400					1405					1410					1415	
	AGA	AGC	CTC	TCC	GAT	AGT	GAC	CTC	CTG	GCT	ATG	AGG	CGG	CAA	GGC	CGC	2132
	Arg	Ser	Leu	Ser	Asp	Ser	Asp	Leu	Leu	Ala	Met	Arg	Arg	Gln	Gly	Arg	
					1420					1425					1430		
40	TTT	CTC	TGG	GAG	ACT	TAC	TTC	TCC	ACT	GCT	GAC	AGT	ATT	TTT	AAT	ACC	2180
	Phe	Leu	Trp	Glu	Thr	Tyr	Phe	Ser	Thr	Ala	Asp	Ser	Ile	Phe	Asn	Thr	
				1435					1440					1445			
	45GTG	CTG	GCT	ATG	ATT	AGG	ACT	CGC	ATC	CAG	ATC	CCA	GCC	GCT	CCC	ATC	2228
	Val	Leu	Ala	Met	Ile	Arg	Thr	Arg	Ile	Gln	Ile	Pro	Ala	Ala	Pro	Ile	
			1450					1455					1460				
	CGG	GAA	GAG	GCG	GCA	GCT	GAG	ATC	CCC	CAC	CGT	TCA	GGC	AAG	GCG	GCT	2276
50	Arg	Glu	Glu	Ala	Ala	Ala	Glu	Ile	Pro	His	Arg	Ser	Gly	Lys	Ala	Ala	
		1465					1470					1475					
	GGA	ACT	GAC	CCC	AAC	ATG	GCT	GAC	AAC	GGG	GAC	CTG	GAC	CTG	GGG	CCA	2324
	Gly	Thr	Asp	Pro	Asn	Met	Ala	Asp	Asn	Gly	Asp	Leu	Asp	Leu	Gly	Pro	
55	1480					1485					1490					1495	
	GTG	GAG	ACG	GAG	CCG	CCC	TAC	GCC	TCA	CCC	AGA	TAC	CTC	CGC	AAT	TTC	2372
	Val	Glu	Thr	Glu	Pro	Pro	Tyr	Ala	Ser	Pro	Arg	Tyr	Leu	Arg	Asn	Phe	
					1500					1505					1510		
60	ACT	CTG	ACT	GTC	ACT	GAC	TTT	TAC	CGC	AGC	TGG	AAC	TGT	GCT	CCA	GGG	2420
	Thr	Leu	Thr	Val	Thr	Asp	Phe	Tyr	Arg	Ser	Trp	Asn	Cys	Ala	Pro	Gly	
				1515				1520						1525			

030920-031601
FOIREF-02650860

	CCT	TTC	CAT	CTT	TTC	CCC	CAC	ACT	CCC	TTT	GAC	CCT	GTG	TTG	CCC	TCA	2468
	Pro	Phe	His	Leu	Phe	Pro	His	Thr	Pro	Phe	Asp	Pro	Val	Leu	Pro	Ser	
			1530					1535					1540				
5	GAG	GCC	AAA	TTC	TTG	GGC	TCA	GGG	ACT	GGC	TTT	CGG	CCT	ATT	GGT	GGT	2516
	Glu	Ala	Lys	Phe	Leu	Gly	Ser	Gly	Thr	Gly	Phe	Arg	Pro	Ile	Gly	Gly	
		1545					1550				1555						
10	GGA	GCT	GGG	GGT	TCT	GGC	AAG	GAA	TTT	CAG	GCA	GCG	CTT	GGA	GGC	AAT	2564
	Gly	Ala	Gly	Gly	Ser	Gly	Lys	Glu	Phe	Gln	Ala	Ala	Leu	Gly	Gly	Asn	
		1560				1565				1570						1575	
15	GTT	CCC	CGA	GAG	CAG	TTC	ACG	GTG	GTG	ATG	TTG	ACT	TAT	GAG	CGG	GAG	2612
	Val	Pro	Arg	Glu	Gln	Phe	Thr	Val	Val	Met	Leu	Thr	Tyr	Glu	Arg	Glu	
					1580					1585					1590		
20	GAA	GTG	CTT	ATG	AAC	TCT	TTA	GAG	AGG	CTG	AAT	GGC	CTC	CCT	TAC	CTG	2660
	Glu	Val	Leu	Met	Asn	Ser	Leu	Glu	Arg	Leu	Asn	Gly	Leu	Pro	Tyr	Leu	
				1595				1600					1605				
25	AAC	AAG	GTC	GTG	GTG	GTG	TGG	AAT	TCT	CCC	AAG	CTG	CCA	TCA	GAG	GAC	2708
	Asn	Lys	Val	Val	Val	Val	Trp	Asn	Ser	Pro	Lys	Leu	Pro	Ser	Glu	Asp	
		1610						1615				1620					
30	CTT	CTG	TGG	CCT	GAC	ATT	GGC	GTT	CCC	ATC	ATG	GTG	GTC	CGT	ACT	GAG	2756
	Leu	Leu	Trp	Pro	Asp	Ile	Gly	Val	Pro	Ile	Met	Val	Val	Arg	Thr	Glu	
		1625					1630				1635						
35	AAG	AAC	AGT	TTG	AAC	AAC	CGA	TTC	TTA	CCC	TGG	AAT	GAA	ATT	GAG	ACA	2804
	Lys	Asn	Ser	Leu	Asn	Asn	Arg	Phe	Leu	Pro	Trp	Asn	Glu	Ile	Glu	Thr	
		1640				1645				1650					1655		
40	GAG	GCC	ATC	CTG	TCC	ATT	GAT	GAC	GAT	GCT	CAC	CTC	CGC	CAT	GAC	GAA	2852
	Glu	Ala	Ile	Leu	Ser	Ile	Asp	Asp	Asp	Ala	His	Leu	Arg	His	Asp	Glu	
				1660				1665					1670				
45	ATC	ATG	TTT	GGG	TTC	CGG	GTG	TGG	AGA	GAA	GCT	CGG	GAC	CGC	ATC	GTG	2900
	Ile	Met	Phe	Gly	Phe	Arg	Val	Trp	Arg	Glu	Ala	Arg	Asp	Arg	Ile	Val	
				1675				1680					1685				
50	GGC	TTC	CCT	GGC	CGT	TAC	CAC	GCA	TGG	GAC	ATC	CCC	CAT	CAG	TCC	TGG	2948
	Gly	Phe	Pro	Gly	Arg	Tyr	His	Ala	Trp	Asp	Ile	Pro	His	Gln	Ser	Trp	
			1690				1695					1700					
55	CTC	TAC	AAC	TCC	AAC	TAC	TCC	TGT	GAG	CTG	TCC	ATG	GTG	CTG	ACA	GGT	2996
	Leu	Tyr	Asn	Ser	Asn	Tyr	Ser	Cys	Glu	Leu	Ser	Met	Val	Leu	Thr	Gly	
		1705					1710				1715						
60	GCT	GCC	TTC	TTT	CAC	AAG	TAT	TAT	GCC	TAC	CTG	TAT	TCT	TAT	GTG	ATG	3044
	Ala	Ala	Phe	Phe	His	Lys	Tyr	Tyr	Ala	Tyr	Leu	Tyr	Ser	Tyr	Val	Met	
		1720				1725				1730					1735		
65	CCC	CAG	GCC	ATC	CGG	GAC	ATG	GTG	GAT	GAA	TAC	ATC	AAC	TGT	GAG	GAC	3092
	Pro	Gln	Ala	Ile	Arg	Asp	Met	Val	Asp	Glu	Tyr	Ile	Asn	Cys	Glu	Asp	
				1740				1745					1750				
70	ATT	GCC	ATG	AAC	TTC	CTT	GTC	TCC	CAC	ATC	ACT	CGG	AAG	CCC	CCC	ATC	3140
	Ile	Ala	Met	Asn	Phe	Leu	Val	Ser	His	Ile	Thr	Arg	Lys	Pro	Pro	Ile	
				1755				1760					1765				
75	AAG	GTG	ACC	TCA	CGG	TGG	ACA	TTC	CGA	TGC	CCA	GGA	TGC	CCT	CAG	GCC	3188
	Lys	Val	Thr	Ser	Arg	Trp	Thr	Phe	Arg	Cys	Pro	Gly	Cys	Pro	Gln	Ala	
		1770						1775				1780					

090920 03160

	CTG TCT CAT GAT GAC TCC CAC TTC CAC GAG CGG CAC AAG TGC ATC AAC	3236
	Leu Ser His Asp Asp Ser His Phe His Glu Arg His Lys Cys Ile Asn	
	1785 1790 1795	
5	TTC TTC GTG AAG GTG TAC GGC TAC ATG CCC CTC CTG TAC ACG CAG TTC	3284
	Phe Phe Val Lys Val Tyr Gly Tyr Met Pro Leu Leu Tyr Thr Gln Phe	
	1800 1805 1810 1815	
	AGG GTG GAT TCT GTG CTC TTC AAG ACA CGC CTG CCC CAT GAC AAG ACC	3332
10	Arg Val Asp Ser Val Leu Phe Lys Thr Arg Leu Pro His Asp Lys Thr	
	1820 1825 1830	
	AAG TGC TTC AAG TTC ATC TAGGGGCAGC GCACGGTCTG GGAAGAGGA	3380
15	Lys Cys Phe Lys Phe Ile	
	1835	
	TGAGCAGAGG GAGGAAGATG GCTCCCAAGG TTCCTAGGCA TTGCAGGACC TTGGGCACAT	3440
	CTGCTGGTGG GTGGCCCAGA GCCTCTGCTG GAAGGGGCAG CAGGAGGAGT GGAAGGAAAC	3500
20	CGCTGCCTTT ATCTTGAAGT CAGCCACACT GGGCCTGGAG CCCTGGGCGG AGTCCCCGGG	3560
	GTTCCCCACA CAGGGCACTG ACTGATAGCT TACACTGAGG ACTGTGGCGA CTCTGCAGAG	3620
25	TCACTCACAC CGTTCGTACG CCCAGGACAG CTGGTTCGTG GTTTTTACAT TCAATAACAA	3680
	CTATTATGAT TATTTAAAAA GAGAAAGTTT CAGATTTGCC ATTCAAGGCT TATTTATATA	3740
	TATGTGTGTG TATATAAATA CATGCACACA CTTGCATACA TATATATTTT TGGCTGGGGG	3800
30	AGTGTGAGTT TTGCCTTTCT AAGGGAGGGA CCGCGCAGGC TCCTTTGTTC TGTATTCTGG	3860
	CGGAGATGGG TCCTGGCCTT GTGTCACCTG CTTATCCTTA AAGATCATCT CCCATCCTCC	3920
35	CCAGCGCCAT CTGTGTGCAG CAACCAGAAA GGGATGAACT TGGCCCTCTT GCGGGCCTGG	3980
	ACAAGGTCTC TTCCTTACCC TTTCTGTTGC CAGTCAGCAA CCTGTAACTC ACATTCTCTT	4040
	CCCAGTGAAT CCCTGGGAGC GCCTGACCCT GGTGGGCTGT TCAGCTTCCT GCTGCTGGGG	4100
40	CCAGCGATTT TTGAGGATTT ATCTTTAGGC CAGGCTTGCC TCCGTA CTTA TCCCTGCTCT	4160
	CCCATTCTC TCTTGTTTGA GAGAGAATGA GGAAGCAAAG AGTGAGAAAAG AATAGGGGCT	4220
45	GAAGACGCCA CTCCCAGATG GCTCTTTCTA TCCTGCTCTT CTGTTGAAAC ACACGTGCTG	4280
	TGGGCCTCAG GCGTTTCTGA AGTGCTCTTT CTTGGATTGG ACAGGAGATC AGCAGCGTGC	4340
	ACATCTGCTG TGGTCTGAAG TGGTTTGCAG GTCAGCCTCC TCTCCCTAGT GTAGAGCAAG	4400
50	CCAGTGCCT TCGAGGAACC CACCCGGCTG GCCGGGAAGT TTTACAGCAA GCGCCTGCC	4460
	TTGGGATAAT TCCTTGGTGA AATTCACCTT CCCCCGCT CTGTCTGGAG CCCATCCTG	4520
55	TGTTATCTGT GGTTTTTTGA CCCCTAATGT CAGCTTGGCT GTAGGACTCC CCGAGGTTTG	4580
	GTATGTGCTA GAACAATGGG AGGCTGTGAT TTGCTGTGTA AGCTCACATC CAGCCTTGA	4640
	ATCTAACGGG CATTCAACAAC CCGAGTTACC ACTTTCCACT CCCTGCTTAG GATTCTGTTC	4700
60	CCTGGGCTGA AACTGAAATA AGCTAATTTT TTGGGTCACG GTGGCAGTAG GGAACCTAG	4760
	GAGGGTGTGA GTGGCATTG TCAGGGATTT AGCCCATGAC GTGTTTCTTG AACCTACTT	4820

0909920 031601

TCTGGAAGTG GAGTTGACTC TGGAAGTTTT CTAGCAACTG AACAAAAGCT CAGGTTTGTC 4880
 CTGGTCATGC ACATGCCTTA AGCCAGTTCC GTCTTCCCTA GACCTTGGCA TCCTGTGCTT 4940
 5CTATTTCTTG GAATACGTTT TCCTCTGACC TGCCTGTACC ACGTGGGTCC TCTTCAAGTA 5000
 CTGTTTTGAA GCTGGGCTCT TTTGTGTAGC TCCCACCCAC CTGTAGGGCT AGCTCGGCTT 5060
 AAGGGAAGTC TCCCCATTGG CAAACCGGAC CCGGCCGCCG CCAGGACTGT GTTTCCAAAG 5120
 10 GTTCCCCGCC CCCAACCCCA GCATCAGCCT GTAGCTCCCC TGCTGAGGCA GTGTGGTTAT 5180
 GTTCCAGCA GTGGGGGTCA GACGCCCTTC CTCAGAACTT TCTAGTTGCC CTCTACCTGA 5240
 15 CTCCTGACTT GTATTCCTTT TAGCAGTAGC CTTCTTCCCT CGGGGAGCCA AAGAGTGTGG 5300
 TGTGTGGCGC TATATTGTGG CTGCTATTTT ATCTGGTTTC TTTAATGTG AGGAACTCAC 5360
 ATACTGACTT CAGTGGGACT CGGTGAGCCG GGGCCGTCTG TGTGGTGGGA CCCCTTTAG 5420
 20 CGGGACTCAG TGAGCTGGGG CCGTCTGTGT GGTGGAGCCA GGGCCTCTCC CTTTAGTGGA 5480
 GCCAGGTTGT CGGGCCCCGA ATGTCACCTG TGGATCTAAG AAGGGCTGAG TGGTCTGACA 5540
 25 CCAAAACATG CCGCAGGGAG GGCTGTGGTG CCGGTGCTTC CAACAAGGAC AGCCCTCCTT 5600
 GACCCTGAAA GGAACACTGG CTTGAAGGAC TGCAGACAGG CTCTGAGGGG CACGCCCTCC 5660
 TCAGCGAGAG GCAGCAAGGT GGCCACAGTG TCACTGGTCA GGTGCTTCTC ACCACGGGAA 5720
 30 AGCCGCCGAC CTGTGACTCG CTTGAGATGG GAAAGCGGCG CCACAGACCC CGGGTCTCCT 5780
 TGGCTGTCTG TGGGCCGCC CTGGCCACCT TGTCTGGCT CGCAGGGTGC AGGAGCGCCT 5840
 35 CGTTCTCTGG GTGGCCGGCT TGCTGCTCCG GTTTGGGCTG TCTTACCATA ACACCGTCCC 5900
 AGGGCTCTGC AGGCCACTGT GAGCGCTGGC TCCCTGGGCA GTGCTCCTCC GTGTGGACTG 5960
 TGCCTCAGGC CAGGGCTCAC CAGCTGGGGT CCTGTCCGGA AGGATGGGAT CTTTCTGGGA 6020
 40 GCTGCGCCGG ACAGAGTGGG GAGCTCCTAG TTTGTGGGGG GAAGCTTTGA TATCCATGCC 6080
 ACGTCCATCC ACCCCACCCC TTTTCGTCAC GAGCACAATG GTCTTACATT GGATTTTTGT 6140
 45 AAAAAAATAA AAATAAATGG AGACTTTAAC TC 6172

(2) INFORMATION FOR SEQ ID NO:4:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 919 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Gly Tyr Thr Met Leu Arg Asn Gly Gly Ala Gly Asn Gly Gly
 60 1 5 10 15
 Gln Thr Cys Met Leu Arg Trp Ser Asn Arg Ile Arg Leu Thr Trp Leu
 20 25 30

FOOTED-02660350

	Ser	Phe	Thr	Leu	Phe	Val	Ile	Leu	Val	Phe	Phe	Pro	Leu	Ile	Ala	His	
			35					40					45				
5	Tyr	Tyr	Leu	Thr	Thr	Leu	Asp	Glu	Ala	Asp	Glu	Ala	Gly	Lys	Arg	Ile	
		50					55					60					
	Phe	Gly	Pro	Arg	Val	Gly	Asn	Glu	Leu	Cys	Glu	Val	Lys	His	Val	Leu	
	65					70					75					80	
10	Asp	Leu	Cys	Arg	Ile	Arg	Glu	Ser	Val	Ser	Glu	Glu	Leu	Leu	Gln	Leu	
					85					90					95		
	Glu	Ala	Lys	Arg	Gln	Glu	Leu	Asn	Ser	Glu	Ile	Ala	Lys	Leu	Asn	Leu	
				100					105					110			
15	Lys	Ile	Glu	Ala	Cys	Lys	Lys	Ser	Ile	Glu	Asn	Ala	Lys	Gln	Asp	Leu	
			115					120					125				
20	Leu	Gln	Leu	Lys	Asn	Val	Ile	Ser	Gln	Thr	Glu	His	Ser	Tyr	Lys	Glu	
	130						135					140					
	Leu	Met	Ala	Gln	Asn	Gln	Pro	Lys	Leu	Ser	Leu	Pro	Ile	Arg	Leu	Leu	
	145					150					155					160	
25	Pro	Glu	Lys	Asp	Asp	Ala	Gly	Leu	Pro	Pro	Pro	Lys	Ala	Thr	Arg	Gly	
				165						170					175		
	Cys	Arg	Leu	His	Asn	Cys	Phe	Asp	Tyr	Ser	Arg	Cys	Pro	Leu	Thr	Ser	
				180					185					190			
30	Gly	Phe	Pro	Val	Tyr	Val	Tyr	Asp	Ser	Asp	Gln	Phe	Val	Phe	Gly	Ser	
			195					200					205				
35	Tyr	Leu	Asp	Pro	Leu	Val	Lys	Gln	Ala	Phe	Gln	Ala	Thr	Ala	Arg	Ala	
	210						215					220					
	Asn	Val	Tyr	Val	Thr	Glu	Asn	Ala	Asp	Ile	Ala	Cys	Leu	Tyr	Val	Ile	
	225					230					235					240	
40	Leu	Val	Gly	Glu	Met	Gln	Glu	Pro	Val	Val	Leu	Arg	Pro	Ala	Glu	Leu	
					245					250					255		
	Glu	Lys	Gln	Leu	Tyr	Ser	Leu	Pro	His	Trp	Arg	Thr	Asp	Gly	His	Asn	
				260					265					270			
45	His	Val	Ile	Ile	Asn	Leu	Ser	Arg	Lys	Ser	Asp	Thr	Gln	Asn	Leu	Leu	
			275					280					285				
50	Tyr	Asn	Val	Ser	Thr	Gly	Arg	Ala	Met	Val	Ala	Gln	Ser	Thr	Phe	Tyr	
	290						295					300					
	Thr	Val	Gln	Tyr	Arg	Pro	Gly	Phe	Asp	Leu	Val	Val	Ser	Pro	Leu	Val	
	305					310					315					320	
55	His	Ala	Met	Ser	Glu	Pro	Asn	Phe	Met	Glu	Ile	Pro	Pro	Gln	Val	Pro	
					325					330					335		
	Val	Lys	Arg	Lys	Tyr	Leu	Phe	Thr	Phe	Gln	Gly	Glu	Lys	Ile	Glu	Ser	
				340					345		</						

Gly Asp Pro Pro Ala Asp Tyr Asp Asp Arg Ile Ile Ala Thr Leu Lys
 370 375 380
 Ala Val Gln Asp Ser Lys Leu Asp Gln Val Leu Val Glu Phe Thr Cys
 5385 390 395 400
 Lys Asn Gln Pro Lys Pro Ser Leu Pro Thr Glu Trp Ala Leu Cys Gly
 405 410 415
 10Glu Arg Glu Asp Arg Leu Glu Leu Leu Lys Leu Ser Thr Phe Ala Leu
 420 425 430
 Ile Ile Thr Pro Gly Asp Pro Arg Leu Val Ile Ser Ser Gly Cys Ala
 435 440 445
 15 Thr Arg Leu Phe Glu Ala Leu Glu Val Gly Ala Val Pro Val Val Leu
 450 455 460
 Gly Glu Gln Val Gln Leu Pro Tyr Gln Asp Met Leu Gln Trp Asn Glu
 20465 470 475 480
 Ala Ala Leu Val Val Pro Lys Pro Arg Val Thr Glu Val His Phe Leu
 485 490 495
 25Leu Arg Ser Leu Ser Asp Ser Asp Leu Leu Ala Met Arg Arg Gln Gly
 500 505 510
 Arg Phe Leu Trp Glu Thr Tyr Phe Ser Thr Ala Asp Ser Ile Phe Asn
 515 520 525
 30 Thr Val Leu Ala Met Ile Arg Thr Arg Ile Gln Ile Pro Ala Ala Pro
 530 535 540
 Ile Arg Glu Glu Ala Ala Ala Glu Ile Pro His Arg Ser Gly Lys Ala
 35545 550 555 560
 Ala Gly Thr Asp Pro Asn Met Ala Asp Asn Gly Asp Leu Asp Leu Gly
 565 570 575
 40Pro Val Glu Thr Glu Pro Pro Tyr Ala Ser Pro Arg Tyr Leu Arg Asn
 580 585 590
 Phe Thr Leu Thr Val Thr Asp Phe Tyr Arg Ser Trp Asn Cys Ala Pro
 595 600 605
 45 Gly Pro Phe His Leu Phe Pro His Thr Pro Phe Asp Pro Val Leu Pro
 610 615 620
 Ser Glu Ala Lys Phe Leu Gly Ser Gly Thr Gly Phe Arg Pro Ile Gly
 50625 630 635 640
 Gly Gly Ala Gly Gly Ser Gly Lys Glu Phe Gln Ala Ala Leu Gly Gly
 645 650 655
 55Asn Val Pro Arg Glu Gln Phe Thr Val Val Met Leu Thr Tyr Glu Arg
 660 665 670
 Glu Glu Val Leu Met Asn Ser Leu Glu Arg Leu Asn Gly Leu Pro Tyr
 675 680 685
 60 Leu Asn Lys Val Val Val Val Trp Asn Ser Pro Lys Leu Pro Ser Glu
 690 695 700

0080920.03101
 TQTEQ.0266060

(2) INFORMATION FOR SEQ ID NO:5:

50 (ii) MOLECULE TYPE: protein

60 Leu Cys Gly Glu Arg Glu Asp Arg Leu Glu Leu Leu Lys Leu Ser Thr
 1 5 10 15

Phe Ala Leu Ile Ile Thr Pro Gly Asp Pro Arg Leu Val Ile Ser Ser
 20 25 30

Gly Cys Ala Thr Arg Leu Phe Glu Ala Leu Glu Val Gly Ala Val Pro
 35 40 45
 Val Val Leu Gly Glu Gln Val Gln Leu Pro Tyr Gln Asp Met Leu Gln
 5 50 55 60
 Trp Asn Glu Ala Ala Leu Val Val Pro Lys Pro Arg Val Thr Glu Val
 65 70 75 80
 His Phe Leu Leu Arg Ser Leu Ser Asp Ser Asp Leu Leu Ala Met Arg
 10 85 90 95
 Arg Gln Gly Arg Phe Leu Trp Glu Thr Tyr Phe Pro Thr Ala Asp Ser
 100 105 110
 Ile Phe Asn Thr Val Leu Ala Met Ile Arg Thr Arg Ile
 15 115 120 125

(2) INFORMATION FOR SEQ ID NO:6:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg Cys His Lys His Gln Val Phe Asp Tyr Pro Gln Val Leu Gln Glu
 35 1 5 10 15
 Ala Thr Phe Cys Val Val Leu Arg Gly Ala Arg Leu Gly Gln Ala Val
 20 25 30
 Leu Ser Asp Val Leu Gln Ala Gly Cys Val Pro Val Val Ile Ala Asp
 40 35 40 45
 Ser Tyr Ile Leu Pro Phe Ser Glu Val Leu Asp Trp Lys Arg Ala Ser
 50 55 60
 Val Val Val Pro Glu Glu Lys Met Ser Asp Val Tyr Ser Ile Leu Gln
 45 65 70 75 80
 Ser Ile Pro Gln Arg Gln Ile Glu Glu Met Gln Arg Gln Ala Arg Trp
 50 85 90 95
 Phe Trp Glu Ala Tyr Phe Gln Ser Ile Lys Ala Ile Ala Leu Ala Thr
 100 105 110
 Leu Gln Ile Ile Asn Asp Arg Ile
 55 115 120

(2) INFORMATION FOR SEQ ID NO:7:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

09809920-031601

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

10 Arg Cys Asp Arg Asp Asn Thr Glu Tyr Glu Lys Tyr Asp Tyr Arg Glu
 1 5 10 15
 Met Leu His Asn Ala Thr Phe Cys Leu Val Pro Arg Gly Arg Arg Leu
 20 25 30
 15 Gly Ser Phe Arg Phe Leu Glu Ala Leu Gln Ala Ala Cys Val Pro Val
 35 40 45
 20 Met Leu Ser Asn Gly Trp Glu Leu Pro Phe Ser Glu Val Ile Asn Trp
 50 55 60
 Asn Gln Ala Ala Val Ile Gly Asp Glu Arg Leu Leu Leu Gln Ile Pro
 65 70 75 80
 25 Ser Thr Ile Arg Ser Ile His Gln Asp Lys Ile Leu Ala Leu Arg Gln
 85 90 95
 Gln Thr Gln Phe Leu Trp Glu Ala Tyr Phe Ser Ser Val Glu Lys Ile
 100 105 110
 30 Val Leu Thr Thr Leu Glu Ile Ile Gln Asp Arg Ile
 115 120

(2) INFORMATION FOR SEQ ID NO:8:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

40

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

50 Arg Cys Glu Gln Asp Pro Gly Pro Gly Gln Thr Gln Arg Gln Glu Thr
 1 5 10 15
 Leu Pro Asn Ala Thr Phe Cys Leu Ile Ser Gly His Arg Pro Glu Ala
 20 25 30
 55 Ala Ser Arg Phe Leu Gln Ala Leu Gln Ala Gly Cys Ile Pro Val Leu
 35 40 45
 Leu Ser Pro Arg Trp Glu Leu Pro Phe Ser Glu Val Ile Asp Trp Thr
 50 55 60
 60 Lys Ala Ala Ile Val Ala Asp Glu Arg Leu Pro Leu Gln Val Leu Ala
 65 70 75 80

TOPIC: 031601

5 Thr Gln Phe Leu Trp Asp Ala Tyr Phe Ser Ser Val Glu Lys Val Ile
100 105 110

His Thr Thr Leu Glu Val Ile Gln Asp Arg Ile
115 120

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20

25	Lys 1	Cys	Ser	Gln	Glu 5	Asn	Cys	Ser	Leu	Glu 10	Arg	Arg	Arg	Gln	Leu 15	Ile
	Gly	Ser	Ser	Thr 20	Phe	Cys	Phe	Leu	Leu 25	Pro	Ser	Glu	Met	Phe 30	Phe	Gln
30	Asp	Phe	Leu 35	Ser	Ser	Leu	Gln	Leu 40	Gly	Cys	Ile	Pro	Ile 45	Leu	Leu	Ser
	Asn	Ser	Gln	Leu	Leu	Pro	Phe 55	Gln	Asp	Leu	Ile	Asp 60	Trp	Arg	Arg	Ala
35	Thr 65	Tyr	Arg	Leu	Pro	Leu 70	Ala	Arg	Leu	Pro	Glu 75	Ala	His	Phe	Ile	Val 80
40	Gln	Ser	Phe	Glu	Ile 85	Ser	Asp	Ile	Ile	Glu 90	Met	Arg	Arg	Val	Gly 95	Arg
	Leu	Phe	Tyr	Glu 100	Thr	Tyr	Leu	Ala	Asp 105	Arg	His	Leu	Leu	Ala 110	Arg	Ser
45	Leu	Leu	Ala 115	Ala	Leu	Arg	Tyr	Lys 120	Leu							

50

55

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Val Pro Arg Glu Gln Phe Thr Val Val Met Leu Thr Tyr Glu Arg Glu
 1 5 10 15
 Glu Val Leu Met Asn Ser Leu Glu Arg Leu Asn Gly Leu Pro Tyr Leu
 5 20 25 30
 Asn Lys Val Val Val Val Trp Asn Ser Pro Lys Leu Pro Ser Glu Asp
 35 40 45
 Leu Leu Trp Pro Asp Ile Gly Val Pro Ile Met Val Val Arg Thr Glu
 10 50 55 60
 Lys Asn Ser Leu Asn Asn Arg Phe Leu Pro Trp Asn Glu Ile Glu Thr
 15 65 70 75 80
 Glu Ala Ile Leu Ser Ile Asp Asp Asp Ala His Leu Arg His Asp Glu
 85 90 95
 Ile Met Phe Gly Phe Arg Val Trp Arg Glu Ala Arg Asp Arg Ile Val
 20 100 105 110
 Gly Phe Pro Gly Arg Tyr His Ala Trp Asp Ile Pro His Gln Ser Trp
 115 120 125
 Leu Tyr Asn Ser Asn Tyr Ser Cys Glu Leu Ser Met Val Leu Thr Gly
 25 130 135 140
 Ala Ala Phe Phe His Lys Tyr Tyr Ala Tyr Leu Tyr Ser Tyr Val Met
 145 150 155 160
 Pro Gln Ala Ile Arg Asp Met Val Asp Glu Tyr Ile Asn Cys Glu Asp
 165 170 175
 Ile Ala Met Asn Phe Leu Val Ser His Ile Thr Arg Lys Pro Pro Ile
 35 180 185 190
 Lys Val Thr Ser Arg Trp Thr Phe Arg Cys Pro Gly Cys Pro Gln Ala
 195 200 205
 Leu Ser His Asp Asp Ser His Phe His Glu Arg His Lys Cys Ile Asn
 40 210 215 220
 Phe Phe Val Lys Val Tyr Gly Tyr Met Pro Leu Leu Tyr Thr Gln Phe
 225 230 235 240
 Arg Val Asp Ser Val Leu Phe Lys Thr Arg Leu Pro His Asp Lys Thr
 245 250 255
 Lys Cys Phe Lys Phe Ile
 50 260

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 55 (A) LENGTH: 269 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 60 (ii) MOLECULE TYPE: protein

FOOTED-02660860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

5 Pro Gln Ser Gln Gly Phe Thr Gln Ile Val Leu Thr Tyr Asp Arg Val
 1 5 10 15
 Glu Ser Leu Phe Arg Val Ile Thr Glu Val Ser Lys Val Pro Ser Leu
 20 25 30
 10 Ser Lys Leu Leu Val Val Trp Asn Asn Gln Asn Lys Asn Pro Pro Glu
 35 40 45
 Asp Ser Leu Trp Pro Lys Ile Arg Val Pro Leu Lys Val Val Arg Thr
 50 55 60
 15 Ala Glu Asn Lys Leu Ser Asn Arg Phe Phe Pro Tyr Asp Glu Ile Glu
 65 70 75 80
 Thr Glu Ala Val Leu Ala Ile Asp Asp Asp Ile Ile Met Leu Thr Ser
 85 90 95
 20 Asp Glu Leu Gln Phe Gly Tyr Glu Val Trp Arg Glu Phe Pro Asp Arg
 100 105 110
 25 Leu Val Gly Tyr Pro Gly Arg Leu His Leu Trp Asp His Glu Ala Met
 115 120 125
 Asn Lys Trp Lys Tyr Glu Ser Glu Trp Thr Asn Glu Val Ser Met Val
 130 135 140
 30 Leu Thr Gly Ala Ala Phe Tyr His Lys Tyr Phe Asn Tyr Leu Tyr Thr
 145 150 155 160
 Lys Met Pro Gly Asp Ile Lys Asn Trp Val Asp Ala His Met Asn Cys
 165 170 175
 35 Tyr Glu Asp Ile Ala Met Asn Phe Leu Val Ala Asn Val Thr Gly Lys
 180 185 190
 40 Ala Val Ile Lys Val Thr Pro Arg Lys Lys Phe Lys Cys Pro Glu Cys
 195 200 205
 Thr Ala Ile Asp Gly Leu Ser Leu Asp Gln Thr His Met Val Glu Arg
 210 215 220
 45 Ser Glu Cys Ile Asn Lys Phe Ala Ser Val Phe Gly Thr Met Pro Leu
 225 230 235 240
 Lys Val Val Glu His Arg Ala Asp Pro Val Leu Tyr Lys Asp Asp Phe
 245 250 255
 50 Pro Glu Lys Leu Lys Ser Phe Pro Asn Ile Gly Ser Leu
 260 265

(2) INFORMATION FOR SEQ ID NO:12:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

60

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

09809920-031601

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

[illegible]

60 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

10

Ser Thr Met Asp Ser Phe Thr Leu Ile Met Gln Thr Tyr Asn Arg Thr
1 5 10 15

15

Asp Leu Leu Leu Lys Leu Leu Asn His Tyr Gln Ala Val Pro Asn Leu
20 25 30

His Lys Val Ile Val Val Trp Asn Asn Ile Gly Glu Lys Ala Pro Asp
35 40 45

20

Glu Leu Trp Asn Ser Leu Gly Pro His Pro Ile Pro Val Ile Phe Lys
50 55 60

Gln Gln Thr Ala Asn Arg Met Arg Asn Arg Leu Gln Val Phe Pro Glu
65 70 75 80

25

Leu Glu Thr Asn Ala Val Leu Met Val Asp Asp Asp Thr Leu Ile Ser
85 90 95

30

Thr Pro Asp Leu Val Phe Ala Phe Ser Val Trp Gln Gln Phe Pro Asp
100 105 110

Gln Ile Val Gly Phe Val Pro Arg Lys His Val Ser Thr Ser Ser Gly
115 120 125

35

Ile Tyr Ser Tyr Gly Ser Phe Glu Met Gln Ala Pro Gly Ser Gly Asn
130 135 140

Gly Asp Gln Tyr Ser Met Val Leu Ile Gly Ala Ser Phe Phe Asn Ser
145 150 155 160

40

Lys Tyr Leu Glu Leu Phe Gln Arg Gln Pro Ala Ala Val His Ala Leu
165 170 175

Ile Asp Asp Thr Gln Asn Cys Asp Asp Ile Ala Met Asn Phe Ile Ile
180 185 190

45

Ala Lys His Ile Gly Lys Thr Ser Gly Ile Phe Val Lys Pro Val Asn
195 200 205

50

Met Asp Asn Leu Glu Lys Glu Thr Asn Ser Gly Tyr Ser Gly Met Trp
210 215 220

His Arg Ala Glu His Ala Leu Gln Arg Ser Tyr Cys Ile Asn Lys Leu
225 230 235 240

55

Val Asn Ile Tyr Asp Ser Met Pro Leu Arg Tyr Ser Asn Ile Met Ile
245 250 255

60

Ser Gln Phe Gly Phe Pro Tyr Ala Asn Tyr Lys Arg Lys Ile
260 265 270

(2) INFORMATION FOR SEQ ID NO:15:

09809920-031601

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

15 Arg Gln Arg Glu Gln Phe Thr Val Val Leu Leu Thr Tyr Glu Arg Asp
 1 5 10 15
 Ala Val Leu Thr Gly Ala Leu Glu Arg Leu His Gln Leu Pro Tyr Leu
 20 20 25 30
 Asn Lys Ile Ile Val Val Trp Asn Asn Val Asn Arg Asp Pro Pro Asp
 35 40 45
 Ser Trp Pro Ser Leu His Ile Pro Val Glu Phe Ile Arg Val Ala Glu
 50 55 60
 25 Asn Asn Leu Asn Asn Arg Phe Val Pro Trp Asp Arg Ile Glu Thr Glu
 65 70 75 80
 Ala Val Leu Ser Leu Asp Asp Asp Ile Asp Leu Met Gln Gln Glu Ile
 85 90 95
 30 Ile Leu Ala Phe Arg Val Trp Arg Glu Asn Arg Asp Arg Ile Val Gly
 100 105 110
 Phe Pro Ala Arg His His Ala Arg Tyr Gly Asp Ser Met Phe Tyr Asn
 115 120 125
 Ser Asn His Thr Cys Gln Met Ser Met Ile Leu Thr Gly Ala Ala Phe
 130 135 140
 40 Ile His Lys Asn Tyr Leu Thr Ala Tyr Thr Tyr Glu Met Pro Ala Glu
 145 150 155 160
 Ile Arg Glu His Val Asn Ser Ile Lys Asn Cys Glu Asp Ile Ala Met
 165 170 175
 45 Asn Tyr Leu Val Ser His Leu Thr Arg Lys Pro Pro Ile Lys Thr Thr
 180 185 190
 Ser Arg Trp Thr Leu Lys Cys Pro Thr Cys Thr Glu Ser Leu Tyr Lys
 195 200 205
 Glu Gly Thr His Phe Glu Lys Arg His Glu Cys Met Arg Leu Phe Thr
 210 215 220
 55 Lys Ile Tyr Gly Tyr Asn Pro Leu Lys Phe Ser Gln Phe Arg Ala Asp
 225 230 235 240
 Ser Ile Leu Phe Lys Thr Arg Leu Pro Gln Asn His Gln Lys Cys Phe
 245 250 255
 60 Lys Tyr Val

05809620-031601
 TOPPED-02660350

(2) INFORMATION FOR SEQ ID NO:16:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTATGGCGAG TGACCCGACG TG

22

20 (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

35TTGCTAAAGT GAAGGAAGTT GG

22

(2) INFORMATION FOR SEQ ID NO:18:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: DNA (genomic)

- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACCCGACGTG ATCTGG

16

(2) INFORMATION FOR SEQ ID NO:19:

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 60 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

09309920-031601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

5AAGAGCTCCT GCAGCTGG

18

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTCTCGTTGC CCTCTCAC

18

(2) INFORMATION FOR SEQ ID NO:21:

25

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATCATCAATC TGTCACG

17

40

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

55

ACTACGATGA CCGGATC

17

(2) INFORMATION FOR SEQ ID NO:23:

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

18

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

16

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40

TATTGGTGGT GGAGCTGG

45

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

60

AATCCAGCCA TGGTCTCCTT GG

22

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGTCGATGCC ATTATTACCA GC

22

15

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA (genomic)

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

30

TTCCTTCCTC ATCACAG

17

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35

40

(ii) MOLECULE TYPE: DNA (genomic)

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGGTCTGTGT ATGCACTTGT G

21

50 (2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: DNA (genomic)

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

05809920-031601

AGTCGATGCC ATTATTACCA GC

22

(2) INFORMATION FOR SEQ ID NO:31:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: DNA (genomic)

- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTCAAGGGTG TGGAGAG

17

20 (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

30

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

35 TTGGCTGAAA GCCAACAACC TG

22

(2) INFORMATION FOR SEQ ID NO:33:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 45 (ii) MOLECULE TYPE: DNA (genomic)

- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AACATGCACG CATCCACAGC

20

(2) INFORMATION FOR SEQ ID NO:34:

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 60 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

"031601" 02660850

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

5TTGTAACACA GCATGTGG

18

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGTTCTGTCA GTATTAGCTG GG

22

(2) INFORMATION FOR SEQ ID NO:36:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTCCTCCCTC TGCTCATCCT C

21

40

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
45 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

55

TTCCCACTCT GTCTCTC

17

"02660860" 031601